08963656 Results

Antibody
SEQ ID NO: 2

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	355	100.0	355	19	AAW51744	Human C-C chemokin
2	308	86.8	355	17	AAW03376	CC-chemokine recep
3	308	86.8	355	18	AAW10100	Human C-C chemokin
4	228	64.2	355	17	AAW03377	CC-chemokine recep
5	228	64.2	355	18	AAW31850	Human eosinophil e
6	228	64.2	355	18	AAW27124	Human chemokine re
7	228	64.2	355	19	AAW51745	Human C-C chemokin
8	228	64.2	355	22	AAG80109	Human CCR3 protein
9	228	64.2	356	18	AAW25943	Human CCKR3 chemok
10	190	53.5	355	22	ABB56341	Non-endogenous hum
11	134	37.7	355	17	AAW03378	CC-chemokine recep
12	134	37.7	355	19	AAW51746	Human C-C chemokin
13	41	11.5	295	22	AAG80106	Human CCR1 protein
14	41	11.5	355	15	AAR52749	C-C chemokine rece
15	41	11.5	355	18	AAW26588	Human MIP-1 alpha/
16	41	11.5	355	18	AAW25751	Human MIP-1alpha/R
17	41	11.5	355	21	AAB20571	Human CC-chemokine

RESULT 15
AAW26588
ID AAW26588 standard; Protein; 355 AA.
XX
AC AAW26588;
XX
DT 21-JAN-1998 (first entry)
XX
DE Human MIP-1 alpha/RANTES receptor.
XX
KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;
KW reduced upon activation normal T expressed and secreted; RANTES;
KW receptor; cytokine; antiinflammatory; inflammation; human.
XX
OS Homo sapiens.
XX
PN US5652133-A.
XX
PD 29-JUL-1997.
XX
PF 28-JAN-1993; 93US-0012988.
XX
PR 28-JAN-1993; 93US-0012988.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Murphy PM;
XX
DR WPI; 1997-392945/36.
DR N-PSDB; AAT90384.
XX
PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop
PT products for the detection of these cytokine(s) and their receptors,
PT particularly in inflammatory processes
XX
PS Claim 2; Column 15-18; 12pp; English.
XX
CC This polypeptide comprises a claimed receptor for human macrophage
CC inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon
CC activation normal T expressed and secreted (RANTES) protein. Also
CC claimed are: a nucleic acid (see AAT90384) that encodes the receptor;
CC a subsequence of the nucleic acid, having at least 12 contiguous

```
CC   nucleotides; a cell transformed or transfected with the nucleic
CC   acid; and purified MIP-1 alpha/RANTES receptor polypeptide.  The
CC   products can be used for detecting the MIP-1 alpha/RANTES receptor
CC   and polymorphisms in physiological samples.  In addition, the
CC   receptor can be expressed and used to assay for MIP-1a/RANTES in
CC   biological samples.  The quantitation of MIP-1 alpha/RANTES is
CC   useful for monitoring the levels of these cytokines in a patient.
CC   Such measurements are useful in following the antiinflammatory
CC   effects of drugs and prospective usefulness of new antiinflammatory
CC   agents.
XX
SQ   Sequence   355 AA;


  Query Match             11.5%;  Score 41;  DB 18;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||
Db    115 tglyseiffiilltidrylaivhavfalrartvtfgvitsi 155


                                    SUMMARIES

Result          %
  No.    Score  Query
                Match Length DB  ID                          Description
 ----------------------------------------------------------------------------
     1      228   64.2    355  4  US-08-575-967A-4            Sequence 4, Appli
     2      228   64.2    355  4  US-08-847-296B-1            Sequence 1, Appli
     3      228   64.2    355  4  US-09-045-583-54            Sequence 54, Appl
     4       41   11.5    355  1  US-08-012-988A-2            Sequence 2, Appli
     5       41   11.5    355  1  US-08-450-393A-5            Sequence 5, Appli
     6       41   11.5    355  4  US-08-446-669-5             Sequence 5, Appli
     7       41   11.5    355  4  US-09-045-583-53            Sequence 53, Appl
     8       41   11.5    355  4  US-09-239-938-1             Sequence 1, Appli
     9       41   11.5    355  5  PCT-US95-00476-5            Sequence 5, Appli
    10       31    8.7     31  1  US-08-450-393A-14           Sequence 14, Appl
    11       31    8.7     31  4  US-08-446-669-14            Sequence 14, Appl
    12       31    8.7     31  5  PCT-US95-00476-14           Sequence 14, Appl
    13       22    6.2     31  1  US-08-450-393A-13           Sequence 13, Appl


RESULT  15
PCT-US95-00476-13
; Sequence 13, Application PC/TUS9500476
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012-2628
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00476
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
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;       REGISTRATION NUMBER:  20,121
;       REFERENCE/DOCKET NUMBER:  5555-291
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  310-977-1001
;       TELEFAX:  310-977-1003
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  31 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
PCT-US95-00476-13


  Query Match              6.2%;  Score 22;  DB 5;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1e-13;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    121 IFFIILLTIDRYLAIVHAVFAL 142
          ||||||||||||||||||||||
Db      1 IFFIILLTIDRYLAIVHAVFAL 22



RESULT  13
US-08-450-393A-13
; Sequence 13, Application US/08450393A
; Patent No. 5707815
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,393A
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  UCAL-237/02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5165
;      TELEFAX:  415-8857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-450-393A-13


  Query Match              6.2%;  Score 22;  DB 1;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1e-13;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    121 IFFIILLTIDRYLAIVHAVFAL 142
          |||||||||||||||||||||||
Db      1 IFFIILLTIDRYLAIVHAVFAL 22
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RESULT 8
US-09-239-938-1
; Sequence 1, Application US/09239938
; Patent No. 6329510
; GENERAL INFORMATION:
; APPLICANT: Qin, Shixin
; APPLICANT: Newman, Walter
; APPLICANT: Kassam, Nasim
; APPLICANT: LeukoSite, Inc.
; TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: LKS97-13
; CURRENT APPLICATION NUMBER: US/09/239,938
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-239-938-1

Query Match 11.5%; Score 41; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	308	86.8	355	2	G02436	chemokine (C-C) re
2	41	11.5	355	2	A45177	chemokine (C-C) re
3	33	9.3	355	2	I49339	macrophage inflamm
4	33	9.3	359	2	I49341	MIP-1 alpha recept
5	22	6.2	360	2	JC2443	chemokine (C-C) re
6	22	6.2	374	2	I38450	chemokine (C-C) re
7	16	4.5	383	2	S55594	G protein-coupled
8	14	3.9	352	2	A43113	chemokine (C-C) re
9	12	3.4	356	2	I49340	MIP-1 alpha recept
10	12	3.4	360	2	A57160	chemokine (C-C) re
11	12	3.4	360	2	JC4587	chemokine (C-C) re
12	10	2.8	308	2	I50241	G protein-coupled

RESULT 9
I49340
MIP-1 alpha receptor like-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49340
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546
A;Accession: I49340
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-356 <RES>
A;Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C;Superfamily: vertebrate rhodopsin

  Query Match   3.4%; Score 12; DB 2; Length 356;
  Best Local Similarity   100.0%; Pred. No. 0.00064;
  Matches   12; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   139 VFALRARTVTFG 150
          ||||||||||||
Db   140 VFALRARTVTFG 151

RESULT 10
A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.;
Wells, T.N.C.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor
cDNA from a human basophilic cell line.
A;Reference number: A57160; MUID:95370289
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Note: source clone K5-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
protein
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match   3.4%; Score 12; DB 2; Length 360;
  Best Local Similarity   100.0%; Pred. No. 0.00065;
  Matches   12; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   72 YLLNLAISDLLF 83
          ||||||||||||
Db   77 YLLNLAISDLLF 88

SEQ ID NO: 6

Result No.	Score	Query Match	Length	DB	ID	Description
1	343	96.6	355	17	AAW03378	CC-chemokine recep
2	343	96.6	355	19	AAW51746	Human C-C chemokin
3	181	51.0	355	17	AAW03376	CC-chemokine recep
4	181	51.0	355	17	AAW03377	CC-chemokine recep
5	181	51.0	355	18	AAW31850	Human eosinophil e
6	181	51.0	355	18	AAW27124	Human chemokine re
7	181	51.0	355	18	AAW10100	Human C-C chemokin
8	181	51.0	355	19	AAW51745	Human C-C chemokin
9	181	51.0	355	22	ABB56341	Non-endogenous hum
10	181	51.0	355	22	AAG80109	Human CCR3 protein
11	181	51.0	356	18	AAW25943	Human CCKR3 chemok
12	134	37.7	355	19	AAW51744	Human C-C chemokin
13	41	11.5	295	22	AAG80106	Human CCR1 protein
14	41	11.5	355	15	AAR52749	C-C chemokine rece
15	41	11.5	355	18	AAW26588	Human MIP-1 alpha/
16	41	11.5	355	18	AAW25751	Human MIP-1alpha/R
17	41	11.5	355	21	AAB20571	Human CC-chemokine
18	34	9.6	34	22	AAG80053	Chemokine peptide
19	31	8.7	31	16	AAR79170	End of third trans

RESULT 14
AAR52749
ID AAR52749 standard; Protein; 355 AA.
XX
AC AAR52749;
XX
DT 30-JAN-1995 (first entry)
XX
DE C-C chemokine receptor.
XX
KW C-C CKR-1; cytokine; inflammation.
XX
OS Homo sapiens.
XX
PN WO9411504-A.
XX
PD 26-MAY-1994.
XX
PF 04-NOV-1993; 93WO-US10672.
XX
PR 10-NOV-1992; 92US-0974025.
XX
PA (GETH) GENENTECH INC.
XX
PI Horuk R, Neote K, Schall T;
XX
DR WPI; 1994-183505/22.
DR N-PSDB; AAQ62695.
XX
PT New C-C chemokine receptor and nucleic acid - are used to develop
PT prods. for use in diagnosis and therapy of inflammation and other
PT cytokine-mediated disorders
XX
PS Claim 1; Fig 9; 90pp; English.
XX
CC The sequence is that of the C-C chemokine receptor. The sequence can
CC be used in therapeutic or diagnostic compsns. for inflammation and
CC other cytokine mediated disorders.
CC See also AAR52750-2.
XX
SQ Sequence 355 AA;

Query Match 11.5%; Score 41; DB 15; Length 355;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||
Db    115 tglyseiffiillltidrylaivhavfalrartvtfgvitsi 155
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RESULT 15
AAW26588
ID AAW26588 standard; Protein; 355 AA.
XX
AC AAW26588;
XX
DT 21-JAN-1998 (first entry)
XX
DE Human MIP-1 alpha/RANTES receptor.
XX
KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;
KW reduced upon activation normal T expressed and secreted; RANTES;
KW receptor; cytokine; antiinflammatory; inflammation; human.
XX
OS Homo sapiens.
XX
PN US5652133-A.
XX
PD 29-JUL-1997.
XX
PF 28-JAN-1993; 93US-0012988.
XX
PR 28-JAN-1993; 93US-0012988.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Murphy PM;
XX
DR WPI; 1997-392945/36.
DR N-PSDB; AAT90384.
XX
PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop
PT products for the detection of these cytokine(s) and their receptors,
PT particularly in inflammatory processes
XX
PS Claim 2; Column 15-18; 12pp; English.
XX
CC This polypeptide comprises a claimed receptor for human macrophage
CC inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon
CC activation normal T expressed and secreted (RANTES) protein. Also
CC claimed are: a nucleic acid (see AAT90384) that encodes the receptor;
CC a subsequence of the nucleic acid, having at least 12 contiguous
CC nucleotides; a cell transformed or transfected with the nucleic
CC acid; and purified MIP-1 alpha/RANTES receptor polypeptide. The
CC products can be used for detecting the MIP-1 alpha/RANTES receptor
CC and polymorphisms in physiological samples. In addition, the
CC receptor can be expressed and used to assay for MIP-1a/RANTES in
CC biological samples. The quantitation of MIP-1 alpha/RANTES is
CC useful for monitoring the levels of these cytokines in a patient.
CC Such measurements are useful in following the antiinflammatory
CC effects of drugs and prospective usefulness of new antiinflammatory
CC agents.
XX
SQ Sequence 355 AA;

Query Match 11.5%; Score 41; DB 18; Length 355;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 tglyseiffiilltidrylaivhavfalrartvtfgvitsi 155
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	181	51.0	355	4	US-08-575-967A-4	Sequence 4, Appli
2	181	51.0	355	4	US-08-847-296B-1	Sequence 1, Appli
3	181	51.0	355	4	US-09-045-583-54	Sequence 54, Appl
4	41	11.5	355	1	US-08-012-988A-2	Sequence 2, Appli
5	41	11.5	355	1	US-08-450-393A-5	Sequence 5, Appli
6	41	11.5	355	4	US-08-446-669-5	Sequence 5, Appli
7	41	11.5	355	4	US-09-045-583-53	Sequence 53, Appl
8	41	11.5	355	4	US-09-239-938-1	Sequence 1, Appli
9	41	11.5	355	5	PCT-US95-00476-5	Sequence 5, Appli
10	31	8.7	31	1	US-08-450-393A-14	Sequence 14, Appl
11	31	8.7	31	4	US-08-446-669-14	Sequence 14, Appl
12	31	8.7	31	5	PCT-US95-00476-14	Sequence 14, Appl
13	22	6.2	31	1	US-08-450-393A-13	Sequence 13, Appl
14	22	6.2	31	4	US-08-446-669-13	Sequence 13, Appl
15	22	6.2	31	5	PCT-US95-00476-13	Sequence 13, Appl
16	22	6.2	344	3	US-08-466-343D-9	Sequence 9, Appli
17	22	6.2	347	1	US-08-461-244-3	Sequence 3, Appli
18	22	6.2	352	3	US-08-466-343D-2	Sequence 2, Appli
19	22	6.2	352	4	US-09-045-583-52	Sequence 52, Appl
20	22	6.2	360	1	US-08-450-393A-4	Sequence 4, Appli

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RESULT   4
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; Sequence 2, Application US/08012988A
; Patent No. 5652133
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Philip M.
;    TITLE OF INVENTION:  Cloning and Expression of Human
;    TITLE OF INVENTION:  Macrophage Inflammatory Protein-1 alpha (MIP-1
;    TITLE OF INVENTION:  alpha)/RANTES Receptor
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94610
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/012,988A
;      FILING DATE:  19930128
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber,, Kenneth A.
;      REGISTRATION NUMBER:  31,677
;      REFERENCE/DOCKET NUMBER:  15280-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  AMINO ACID
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-012-988A-2


  Query Match             11.5%;  Score 41;  DB 1;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-31;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155



RESULT   5
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,393A
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  UCAL-237/02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5165
;      TELEFAX:  415-8857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-450-393A-5


  Query Match             11.5%;  Score 41;  DB 1;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-31;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
```

```
RESULT  12
PCT-US95-00476-14
; Sequence 14, Application PC/TUS9500476
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012-2628
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00476
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-291
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  310-977-1001
;      TELEFAX:  310-977-1003
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-00476-14
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Query Match 8.7%; Score 31; DB 5; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     121 IFFIILLTIDRYLAIVHAVFALRARTVTFGV 151
           |||||||||||||||||||||||||||||||
Db       1 IFFIILLTIDRYLAIVHAVFALRARTVTFGV 31
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	181	51.0	355	1	CKR3_HUMAN	P51677 homo sapien
2	64	18.0	355	1	CKR3_MACMU	P56483 macaca mula
3	55	15.5	355	1	CKR3_CERAE	P56492 cercopithec
4	41	11.5	355	1	CKR1_HUMAN	P32246 homo sapien
5	41	11.5	355	1	CKR1_MACMU	P56482 macaca mula
6	33	9.3	355	1	CKR1_MOUSE	P51675 mus musculu
7	33	9.3	359	1	CKR3_MOUSE	P51678 mus musculu
8	29	8.2	358	1	CKR3_CAVPO	Q9z2i3 cavia porce
9	23	6.5	359	1	CKR3_RAT	O54814 rattus norv
10	22	6.2	352	1	CKR5_CERAE	P56493 cercopithec
11	22	6.2	352	1	CKR5_CERTO	O62743 cercocebus
12	22	6.2	352	1	CKR5_GORGO	P56439 gorilla gor
13	22	6.2	352	1	CKR5_HYLLE	O97883 hylobates l
14	22	6.2	352	1	CKR5_MACMU	P79436 macaca mula

```
RESULT   4
CKR1_HUMAN
ID   CKR1_HUMAN     STANDARD;      PRT;   355 AA.
AC   P32246;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1)
DE   (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE   (RANTES-R) (HM145) (LD78 receptor).
GN   CCR1 OR CMKBR1 OR CMKR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93161416; PubMed=7679328;
RA   Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
RT   "Molecular cloning, functional expression, and signaling
RT   characteristics of a C-C chemokine receptor.";
RL   Cell 72:415-425(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93240122; PubMed=7683036;
RA   Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
RA   Murphy P.M.;
RT   "Structure and functional expression of the human macrophage
RT   inflammatory protein 1 alpha/RANTES receptor.";
RL   J. Exp. Med. 177:1421-1427(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Monocytes;
RX   MEDLINE=94092629; PubMed=7505609;
RA   Nomura H., Nielsen B.W., Matsushima K.;
RT   "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT   leukocyte chemotactic peptide receptors.";
RL   Int. Immunol. 5:1239-1249(1993).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1 DELTA, RANTES, AND MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-
CC       BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING
CC       THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING
CC       STEM CELL PROLIFERATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT HEMATOPOIETIC
CC       CELLS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L09230; AAA58408.1; -.
DR   EMBL; L10918; AAA36543.1; -.
DR   EMBL; D10925; BAA01723.1; -.
DR   PIR; A45177; A45177.
DR   GCRDb; GCR_0498; -.
DR   GCRDb; GCR_0557; -.
DR   GCRDb; GCR_0573; -.
DR   MIM; 601159; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
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FT   DOMAIN        1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     60       1 (POTENTIAL).
FT   DOMAIN       61     64       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     65     91       2 (POTENTIAL).
FT   DOMAIN       92    107       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    108    129       3 (POTENTIAL).
FT   DOMAIN      130    146       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    147    171       4 (POTENTIAL).
FT   DOMAIN      172    197       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    198    223       5 (POTENTIAL).
FT   DOMAIN      224    239       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    240    264       6 (POTENTIAL).
FT   DOMAIN      265    281       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    282    305       7 (POTENTIAL).
FT   DOMAIN      306    355       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    106    183       BY SIMILARITY.
FT   CONFLICT    337    337       E -> D (IN REF. 3).
SQ   SEQUENCE   355 AA;  41172 MW;  B2C100FFED275985 CRC64;


  Query Match             11.5%;  Score 41;  DB 1;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-31;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155


RESULT   7
CKR3_MOUSE
ID   CKR3_MOUSE     STANDARD;      PRT;   359 AA.
AC   P51678;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Probable C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)
DE   (CCR3) (CKR3) (Macrophage inflammatory protein-1 alpha receptor-like
DE   2) (MIP-1 alpha RL2).
GN   CCR3 OR CMKBR3 OR CMKBR1L2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=96072806; PubMed=7594543;
RA   Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA   Gerard C.;
RT   "Molecular characterization of two murine eosinophil beta chemokine
RT   receptors.";
RL   J. Immunol. 155:5299-5305(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SVJ;
RX   MEDLINE=95340546; PubMed=7542241;
RA   Gao J.-L., Murphy P.M.;
RT   "Cloning and differential tissue-specific expression of three mouse
RT   beta chemokine receptor-like genes, including the gene for a
RT   functional macrophage inflammatory protein-1 alpha receptor.";
RL   J. Biol. Chem. 270:17494-17501(1995).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
CC       MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: DETECTED IN SKELETAL MUSCLE AND IN TRACE
CC       AMOUNTS IN LEUKOCYTES.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
```

```
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U29677; AAA86118.1; -.
DR   EMBL; U28406; AAA89155.1; -.
DR   GCRDb; GCR_1673; -.
DR   GCRDb; GCR_1695; -.
DR   MGD; MGI:104616; Cmkbr112.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane.
FT   DOMAIN        1     38       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     39     64       1 (POTENTIAL).
FT   DOMAIN       65     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     95       2 (POTENTIAL).
FT   DOMAIN       96    111       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    112    133       3 (POTENTIAL).
FT   DOMAIN      134    150       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    151    175       4 (POTENTIAL).
FT   DOMAIN      176    201       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    202    227       5 (POTENTIAL).
FT   DOMAIN      228    243       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    244    268       6 (POTENTIAL).
FT   DOMAIN      269    285       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    286    309       7 (POTENTIAL).
FT   DOMAIN      310    359       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    110    187       BY SIMILARITY.
FT   CONFLICT    270    270       R -> S (IN REF. 2).
SQ   SEQUENCE   359 AA;  41825 MW;  AC11ED66E283CEAF CRC64;


  Query Match             9.3%;  Score 33;  DB 1;  Length 359;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-23;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    117 LYSEIFFIILLTIDRYLAIVHAVFALRARTVTF 149
          |||||||||||||||||||||||||||||||||
Db    121 LYSEIFFIILLTIDRYLAIVHAVFALRARTVTF 153
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	72	20.3	72	4	Q96T96	Q96t96 homo sapien
2	56	15.8	56	4	Q96T97	Q96t97 homo sapien
3	51	14.4	355	6	Q9BDS8	Q9bds8 macaca fasc
4	41	11.5	355	6	Q9MYJ8	Q9myj8 callithrix
5	35	9.9	355	11	Q91VP9	Q91vp9 mus musculu
6	35	9.9	358	6	Q9N0M0	Q9n0m0 ovis aries
7	26	7.3	351	6	Q9MYJ9	Q9myj9 oryctolagus
8	25	7.0	355	11	Q9JLY8	Q9jly8 rattus norv
9	22	6.2	316	6	Q9TUV7	Q9tuv7 saguinus sp
10	22	6.2	334	6	Q9TUQ7	Q9tuq7 erythrocebu
11	22	6.2	339	6	Q9TQX3	Q9tqx3 mandrillus
12	22	6.2	339	6	Q9TQX2	Q9tqx2 erythrocebu
13	22	6.2	339	6	Q9TQW4	Q9tqw4 pan troglod
14	22	6.2	339	6	Q9TQW2	Q9tqw2 pongo pygma
15	22	6.2	339	6	Q9TQW0	Q9tqw0 hylobates c

16	22	6.2	339	6	Q9TQV6	Q9tqv6 colobus gue
17	22	6.2	339	6	Q9TQV5	Q9tqv5 saguinus sp
18	22	6.2	339	6	Q9TQV3	Q9tqv3 cercopithec

16	22	6.2	339	6	Q9TQV6	Q9tqv6 colobus gue
17	22	6.2	339	6	Q9TQV5	Q9tqv5 saguinus sp
18	22	6.2	339	6	Q9TQV3	Q9tqv3 cercopithec

SEQ ID NO: 4

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	355	100.0	355	17	AAW03377	CC-chemokine recep
2	355	100.0	355	18	AAW31850	Human eosinophil e
3	355	100.0	355	18	AAW27124	Human chemokine re
4	355	100.0	355	19	AAW51745	Human C-C chemokin
5	355	100.0	355	22	AAG80109	Human CCR3 protein
6	281	79.2	356	18	AAW25943	Human CCKR3 chemok
7	275	77.5	355	17	AAW03376	CC-chemokine recep
8	275	77.5	355	18	AAW10100	Human C-C chemokin
9	254	71.5	355	22	ABB56341	Non-endogenous hum
10	228	64.2	355	19	AAW51744	Human C-C chemokin
11	181	51.0	355	17	AAW03378	CC-chemokine recep
12	181	51.0	355	19	AAW51746	Human C-C chemokin
13	41	11.5	295	22	AAG80106	Human CCR1 protein
14	41	11.5	355	15	AAR52749	C-C chemokine rece
15	41	11.5	355	18	AAW26588	Human MIP-1 alpha/
16	41	11.5	355	18	AAW25751	Human MIP-1alpha/R
17	41	11.5	355	21	AAB20571	Human CC-chemokine
18	34	9.6	34	22	AAG80053	Chemokine peptide
19	32	9.0	32	22	AAG80082	Chemokine CCR3 ext
20	31	8.7	31	16	AAR79170	End of third trans
21	27	7.6	28	20	AAY39255	G-protein coupled
22	26	7.3	28	20	AAY39256	G-protein coupled

RESULT 14
AAR52749
ID AAR52749 standard; Protein; 355 AA.
XX
AC AAR52749;
XX
DT 30-JAN-1995 (first entry)
XX
DE C-C chemokine receptor.
XX
KW C-C CKR-1; cytokine; inflammation.
XX
OS Homo sapiens.
XX
PN WO9411504-A.
XX
PD 26-MAY-1994.
XX
PF 04-NOV-1993; 93WO-US10672.
XX
PR 10-NOV-1992; 92US-0974025.
XX
PA (GETH) GENENTECH INC.
XX
PI Horuk R, Neote K, Schall T;
XX
DR WPI; 1994-183505/22.
DR N-PSDB; AAQ62695.
XX
PT New C-C chemokine receptor and nucleic acid - are used to develop
PT prods. for use in diagnosis and therapy of inflammation and other
PT cytokine-mediated disorders
XX
PS Claim 1; Fig 9; 90pp; English.
XX

CC The sequence is that of the C-C chemokine receptor. The sequence can
CC be used in therapeutic or diagnostic compsns. for inflammation and
CC other cytokine mediated disorders.
CC See also AAR52750-2.
XX
SQ Sequence 355 AA;

Query Match 11.5%; Score 41; DB 15; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
||||||||||||||||||||||||||||||||||||||||
Db 115 tglyseiffiillltidrylaivhavfalrartvtfgvitsi 155

RESULT 15
AAW26588
ID AAW26588 standard; Protein; 355 AA.
XX
AC AAW26588;
XX
DT 21-JAN-1998 (first entry)
XX
DE Human MIP-1 alpha/RANTES receptor.
XX
KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;
KW reduced upon activation normal T expressed and secreted; RANTES;
KW receptor; cytokine; antiinflammatory; inflammation; human.
XX
OS Homo sapiens.
XX
PN US5652133-A.
XX
PD 29-JUL-1997.
XX
PF 28-JAN-1993; 93US-0012988.
XX
PR 28-JAN-1993; 93US-0012988.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Murphy PM;
XX
DR WPI; 1997-392945/36.
DR N-PSDB; AAT90384.
XX
PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop
PT products for the detection of these cytokine(s) and their receptors,
PT particularly in inflammatory processes
XX
PS Claim 2; Column 15-18; 12pp; English.
XX
CC This polypeptide comprises a claimed receptor for human macrophage
CC inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon
CC activation normal T expressed and secreted (RANTES) protein. Also
CC claimed are: a nucleic acid (see AAT90384) that encodes the receptor;
CC a subsequence of the nucleic acid, having at least 12 contiguous
CC nucleotides; a cell transformed or transfected with the nucleic
CC acid; and purified MIP-1 alpha/RANTES receptor polypeptide. The
CC products can be used for detecting the MIP-1 alpha/RANTES receptor
CC and polymorphisms in physiological samples. In addition, the
CC receptor can be expressed and used to assay for MIP-1a/RANTES in
CC biological samples. The quantitation of MIP-1 alpha/RANTES is
CC useful for monitoring the levels of these cytokines in a patient.
CC Such measurements are useful in following the antiinflammatory
CC effects of drugs and prospective usefulness of new antiinflammatory
CC agents.
XX

SQ Sequence 355 AA;

  Query Match 11.5%; Score 41; DB 18; Length 355;
  Best Local Similarity 100.0%; Pred. No. 1.2e-31;
  Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||
Db    115 tglyseiffiilltidrylaivhavfalrartvtfgvitsi 155
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	355	100.0	355	4	US-08-575-967A-4	Sequence 4, Appli
2	355	100.0	355	4	US-08-847-296B-1	Sequence 1, Appli
3	355	100.0	355	4	US-09-045-583-54	Sequence 54, Appl
4	41	11.5	355	1	US-08-012-988A-2	Sequence 2, Appli
5	41	11.5	355	1	US-08-450-393A-5	Sequence 5, Appli
6	41	11.5	355	4	US-08-446-669-5	Sequence 5, Appli
7	41	11.5	355	4	US-09-045-583-53	Sequence 53, Appl
8	41	11.5	355	4	US-09-239-938-1	Sequence 1, Appli
9	41	11.5	355	5	PCT-US95-00476-5	Sequence 5, Appli
10	31	8.7	31	1	US-08-450-393A-14	Sequence 14, Appl
11	31	8.7	31	4	US-08-446-669-14	Sequence 14, Appl
12	31	8.7	31	5	PCT-US95-00476-14	Sequence 14, Appl
13	22	6.2	31	1	US-08-450-393A-13	Sequence 13, Appl
14	22	6.2	31	4	US-08-446-669-13	Sequence 13, Appl
15	22	6.2	31	5	PCT-US95-00476-13	Sequence 13, Appl
16	22	6.2	344	3	US-08-466-343D-9	Sequence 9, Appli
17	22	6.2	347	1	US-08-461-244-3	Sequence 3, Appli
18	22	6.2	352	3	US-08-466-343D-2	Sequence 2, Appli

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RESULT  4
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Philip M.
;    TITLE OF INVENTION:  Cloning and Expression of Human
;    TITLE OF INVENTION:  Macrophage Inflammatory Protein-1 alpha (MIP-1
;    TITLE OF INVENTION:  alpha)/RANTES Receptor
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94610
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/012,988A
;      FILING DATE:  19930128
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber,, Kenneth A.
;      REGISTRATION NUMBER:  31,677
;      REFERENCE/DOCKET NUMBER:  15280-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
```

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;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-012-988A-2


  Query Match             11.5%;  Score 41;  DB 1;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-31;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155



RESULT   5
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,393A
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  UCAL-237/02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5165
;      TELEFAX:  415-8857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-450-393A-5


  Query Match             11.5%;  Score 41;  DB 1;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-31;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
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RESULT   9
PCT-US95-00476-5
; Sequence 5, Application PC/TUS9500476
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012-2628
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00476
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-291
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  310-977-1001
;      TELEFAX:  310-977-1003
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US95-00476-5


  Query Match             11.5%;  Score 41;  DB 5;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-31;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	275	77.5	355	2	G02436	chemokine (C-C) re
2	41	11.5	355	2	A45177	chemokine (C-C) re
3	33	9.3	355	2	I49339	macrophage inflamm
4	33	9.3	359	2	I49341	MIP-1 alpha recept
5	22	6.2	360	2	JC2443	chemokine (C-C) re
6	22	6.2	374	2	I38450	chemokine (C-C) re
7	16	4.5	383	2	S55594	G protein-coupled
8	14	3.9	352	2	A43113	chemokine (C-C) re
9	12	3.4	356	2	I49340	MIP-1 alpha recept
10	12	3.4	360	2	A57160	chemokine (C-C) re

11	12	3.4	360	2	JC4587	chemokine (C-C) re
12	10	2.8	308	2	I50241	G protein-coupled
13	10	2.8	327	2	S56162	MDCR15 protein - h
14	10	2.8	355	2	JC5067	G protein-coupled
15	10	2.8	372	2	S26667	G protein-coupled
16	10	2.8	374	2	S42628	G protein-coupled
17	10	2.8	374	2	S32785	G protein-coupled
18	9	2.5	177	2	PH1372	angiotensin II rec
19	9	2.5	350	2	A39445	interleukin-8 rece
20	9	2.5	352	2	G00048	fusin (LESTRA) - c

```
RESULT   1
G02436
chemokine (C-C) receptor 3 - human
N;Alternate names: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C;Accession: G02436; A57237
R;Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A;Reference number: H01272
A;Accession: G02436
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <PON>
A;Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561
R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A;Reference number: A57237; MUID:95348056
A;Accession: A57237
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0,
PIDN:AAC50469.1, differs from the published sequence in having 281-Leu
C;Genetics:
A;Gene: GDB:CMKBR3
A;Cross-references: GDB:579624; OMIM:601268
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
protein
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-261/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted


  Query Match             77.5%;  Score 275;  DB 2;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-273;
  Matches  275;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTTSLDTVETFGTTSYYDDVGLLCEKADTRALMAQFVPPLYSLVFTVGLLGNVVVVMILI 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTTSLDTVETFGTTSYYDDVGLLCEKADTRALMAQFVPPLYSLVFTVGLLGNVVVVMILI 60

Qy      61 KYRRLRIMTNIYLLNLAISDLLFLVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 KYRRLRIMTNIYLLNLAISDLLFLVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSE 120
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Qy    121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEE 180

Qy    181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVLPLLVMAICYTGIIKTLLRCPSKKKYKAIRL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVLPLLVMAICYTGIIKTLLRCPSKKKYKAIRL 240

Qy    241 IFVIMAVFFIFWTPYNVAILLSSYQSILFGNDCER 275
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Db    241 IFVIMAVFFIFWTPYNVAILLSSYQSILFGNDCER 275
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RESULT 2
A45177
chemokine (C-C) receptor 1 - human
N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: A45177; I55671
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.
A;Reference number: A45177; MUID:93161416
A;Accession: A45177
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-355 <NEO>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.
A;Reference number: I55671; MUID:93240122
A;Accession: I55671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355 <RES>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C;Genetics:
A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

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  Query Match             11.5%;  Score 41;  DB 2;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-33;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
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RESULT 3
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49339
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.
A;Reference number: I49339; MUID:95340546
A;Accession: I49339
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <RES>
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C;Superfamily: vertebrate rhodopsin

Query Match 9.3%; Score 33; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.9e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GLYSEIFFIILLTIDRYLAIVHAVFALRARTVT 148
||||||||||||||||||||||||||||||||||
Db 116 GLYSEIFFIILLTIDRYLAIVHAVFALRARTVT 148

RESULT 5
JC2443
chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor.
A;Reference number: JC2443; MUID:94324942
A;Accession: JC2443
A;Molecule type: mRNA
A;Residues: 1-360 <YAM>
A;Cross-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.
A;Reference number: A53477; MUID:94195821
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>

F;207-226/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;287-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;113-190/Disulfide bonds: #status predicted

Query Match 6.2%; Score 22; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121 IFFIILLTIDRYLAIVHAVFAL 142
          ||||||||||||||||||||||
Db    128 IFFIILLTIDRYLAIVHAVFAL 149
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RESULT 6
I38450
chemokine (C-C) receptor 2, splice form A - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C;Accession: I38450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.
A;Reference number: A53477; MUID:94195821
A;Accession: I38450
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <RES>
A;Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F;44-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;244-265/Domain: transmembrane #status predicted <TM6>
F;292-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;32-277,113-190/Disulfide bonds: #status predicted

Query Match 6.2%; Score 22; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.8e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121 IFFIILLTIDRYLAIVHAVFAL 142
          ||||||||||||||||||||||
Db    128 IFFIILLTIDRYLAIVHAVFAL 149
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	355	100.0	355	1	CKR3_HUMAN	P51677 homo sapien
2	64	18.0	355	1	CKR3_MACMU	P56483 macaca mula
3	55	15.5	355	1	CKR3_CERAE	P56492 cercopithec

4	41	11.5	355	1	CKR1_HUMAN	P32246	homo sapien
5	41	11.5	355	1	CKR1_MACMU	P56482	macaca mula
6	33	9.3	355	1	CKR1_MOUSE	P51675	mus musculu
7	33	9.3	359	1	CKR3_MOUSE	P51678	mus musculu
8	29	8.2	358	1	CKR3_CAVPO	Q9z2i3	cavia porce
9	23	6.5	359	1	CKR3_RAT	O54814	rattus norv
10	22	6.2	352	1	CKR5_CERAE	P56493	cercopithec
11	22	6.2	352	1	CKR5_CERTO	O62743	cercocebus
12	22	6.2	352	1	CKR5_GORGO	P56439	gorilla gor
13	22	6.2	352	1	CKR5_HYLLE	O97883	hylobates l
14	22	6.2	352	1	CKR5_MACMU	P79436	macaca mula
15	22	6.2	352	1	CKR5_PANTR	P56440	pan troglod
16	22	6.2	352	1	CKR5_PAPHA	P56441	papio hamad
17	22	6.2	352	1	CKR5_PONPY	O97881	pongo pygma
18	22	6.2	352	1	CKR5_PYGBI	O97880	pygathrix b

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RESULT   4
CKR1_HUMAN
ID   CKR1_HUMAN     STANDARD;      PRT;   355 AA.
AC   P32246;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1)
DE   (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE   (RANTES-R) (HM145) (LD78 receptor).
GN   CCR1 OR CMKBR1 OR CMKR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93161416; PubMed=7679328;
RA   Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
RT   "Molecular cloning, functional expression, and signaling
RT   characteristics of a C-C chemokine receptor.";
RL   Cell 72:415-425(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93240122; PubMed=7683036;
RA   Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
RA   Murphy P.M.;
RT   "Structure and functional expression of the human macrophage
RT   inflammatory protein 1 alpha/RANTES receptor.";
RL   J. Exp. Med. 177:1421-1427(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Monocytes;
RX   MEDLINE=94092629; PubMed=7505609;
RA   Nomura H., Nielsen B.W., Matsushima K.;
RT   "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT   leukocyte chemotactic peptide receptors.";
RL   Int. Immunol. 5:1239-1249(1993).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       MIP-1 DELTA, RANTES, AND MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-
CC       BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING
CC       THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING
CC       STEM CELL PROLIFERATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT HEMATOPOIETIC
CC       CELLS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; L09230; AAA58408.1; -.
DR   EMBL; L10918; AAA36543.1; -.
DR   EMBL; D10925; BAA01723.1; -.
DR   PIR; A45177; A45177.
DR   GCRDb; GCR_0498; -.
DR   GCRDb; GCR_0557; -.
DR   GCRDb; GCR_0573; -.
DR   MIM; 601159; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     60       1 (POTENTIAL).
FT   DOMAIN       61     64       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     65     91       2 (POTENTIAL).
FT   DOMAIN       92    107       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    108    129       3 (POTENTIAL).
FT   DOMAIN      130    146       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    147    171       4 (POTENTIAL).
FT   DOMAIN      172    197       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    198    223       5 (POTENTIAL).
FT   DOMAIN      224    239       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    240    264       6 (POTENTIAL).
FT   DOMAIN      265    281       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    282    305       7 (POTENTIAL).
FT   DOMAIN      306    355       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    106    183       BY SIMILARITY.
FT   CONFLICT    337    337       E -> D (IN REF. 3).
SQ   SEQUENCE   355 AA;  41172 MW;  B2C100FFED275985 CRC64;


  Query Match             11.5%;  Score 41;  DB 1;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-31;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
          |||||||||||||||||||||||||||||||||||||||||||
Db    115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155



RESULT   6
CKR1_MOUSE
ID   CKR1_MOUSE     STANDARD;      PRT;   355 AA.
AC   P51675;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1)
DE   (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE   (RANTES-R).
GN   CCR1 OR CMKBR1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=Peritoneal macrophage;
RX   MEDLINE=96072806; PubMed=7594543;
RA   Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA   Gerard C.;
RT   "Molecular characterization of two murine eosinophil beta chemokine
```

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RT   receptors.";
RL   J. Immunol. 155:5299-5305(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SVJ;
RX   MEDLINE=95340546; PubMed=7542241;
RA   Gao J.-L., Murphy P.M.;
RT   "Cloning and differential tissue-specific expression of three mouse
RT   beta chemokine receptor-like genes, including the gene for a
RT   functional macrophage inflammatory protein-1 alpha receptor.";
RL   J. Biol. Chem. 270:17494-17501(1995).
CC   -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC       RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC       SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC       CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC       PROLIFERATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: DETECTED IN THE HEART, SPLEEN, LUNG,
CC       PERITONEAL EXUDATE CELLS AND LEUKOCYTES.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U29678; AAA86119.1; -.
DR   EMBL; U28404; AAA89153.1; -.
DR   GCRDb; GCR_1672; -.
DR   GCRDb; GCR_1698; -.
DR   MGD; MGI:104618; Cmkbr1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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FT   DOMAIN       61     64       CYTOPLASMIC (POTENTIAL).
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FT   TRANSMEM    108    129       3 (POTENTIAL).
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FT   TRANSMEM    147    171       4 (POTENTIAL).
FT   DOMAIN      172    197       EXTRACELLULAR (POTENTIAL).
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FT   DOMAIN      265    281       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    282    305       7 (POTENTIAL).
FT   DOMAIN      306    355       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    106    183       BY SIMILARITY.
FT   CONFLICT     55     55       M -> V (IN REF. 2).
SQ   SEQUENCE   355 AA;  40901 MW;  FCE9FFF70E6F38B1 CRC64;


  Query Match             9.3%;  Score 33;  DB 1;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    116 GLYSEIFFIILLTIDRYLAIVHAVFALRARTVT 148
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Db    116 GLYSEIFFIILLTIDRYLAIVHAVFALRARTVT 148
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